

10664423-3vssc1a_rat.txt

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 5, 2008, 12:26:52 ; Search time 1 Seconds
(without alignments)
4.036 Million cell updates/sec

Title: us-10-664-423a-3
Perfect score: 10403
Sequence: 1 MEQTVLVPPGPDSFNFFTRE.....TKPI VEKHEQEGKDEKAKGK 2009

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 2009 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : scn1a_rat.uni prot_sprot: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10258	98.6	2009	1	SCN1A_RAT	Sodium channel pro

ALIGNMENTS

RESULT 1

SCN1A_RAT

ID SCN1A_RAT STANDARD; PRT; 2009 AA.
AC P04774;
DT 13-AUG-1987, integrated into UniProt KB/ Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 27-JUN-2006, entry version 67.
DE Sodium channel protein type 1 subunit alpha (Sodium channel protein type I subunit alpha) (Voltage-gated sodium channel subunit alpha Nav1.1) (Sodium channel protein, brain I subunit alpha).
GN Name=Scn1a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=86146901; PubMed=3754035; DOI=10.1038/320188a0;
RA Noda M, Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M,
RA Takahashi H., Numa S.;
RT "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL Nature 320:188-192(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=87311395; PubMed=2442385;
RA Noda M., Numa S.;
RT "Structure and function of sodium channel.";
RL J. Recept. Res. 7:467-497(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 177-253.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92051314; PubMed=1658739;
RA Sarao R., Gupta S.K., Auld V.J., Dunn R.J.;
RT "Developmentally regulated alternative RNA splicing of rat brain
RT sodium channel mRNAs.";
RL Nucleic Acids Res. 19:5673-5679(1991).
CC -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -!- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- SIMILARITY: Belongs to the sodium channel family.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC -----
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CC -----
DR EMBL; X03638; CAA27286.1; -; mRNA.
DR EMBL; M22253; AAA79965.1; -; mRNA.
DR PIR; A25019; A25019.
DR UniGene; Rn.32079; -.
DR HSSP; P04775; 1BYY.
DR RGD; 69364; Scn1a.
DR GO; GO:0005248; F: voltage-gated sodium channel activity; TAS.
DR GO; GO:0019228; P: generation of action potential; TAS.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR011992; EF-Hand_type.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_CaM_bd_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008051; Na_channel1.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01664; NACHANNEL1.
DR PROSITE; PS00096; IQ_FALSE_NEG.
KW Glycoprotein; Ion transport; Ionic channel; Membrane; Repeat; Sodium

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KW Sodi um channel ; Sodi um t ransport ; Transmembrane; Transport ;
 KW Voltage-gated channel .
 FT CHAI N 1 2009 Sodi um channel protei n type 1 subunit
 FT al pha.
 FT / FTI d=PRO_0000048490.
 FT TRANSMEM 124 147 S1 of repeat I .
 FT TRANSMEM 156 175 S2 of repeat I .
 FT TRANSMEM 189 207 S3 of repeat I .
 FT TRANSMEM 214 233 S4 of repeat I .
 FT TRANSMEM 250 273 S5 of repeat I .
 FT TRANSMEM 400 425 S6 of repeat I .
 FT TRANSMEM 763 787 S1 of repeat II .
 FT TRANSMEM 799 822 S2 of repeat II .
 FT TRANSMEM 831 850 S3 of repeat II .
 FT TRANSMEM 857 876 S4 of repeat II .
 FT TRANSMEM 893 913 S5 of repeat II .
 FT TRANSMEM 967 992 S6 of repeat II .
 FT TRANSMEM 1214 1237 S1 of repeat III .
 FT TRANSMEM 1251 1276 S2 of repeat III .
 FT TRANSMEM 1283 1304 S3 of repeat III .
 FT TRANSMEM 1309 1330 S4 of repeat III .
 FT TRANSMEM 1350 1377 S5 of repeat III .
 FT TRANSMEM 1457 1483 S6 of repeat III .
 FT TRANSMEM 1537 1560 S1 of repeat IV .
 FT TRANSMEM 1572 1595 S2 of repeat IV .
 FT TRANSMEM 1602 1625 S3 of repeat IV .
 FT TRANSMEM 1636 1657 S4 of repeat IV .
 FT TRANSMEM 1673 1695 S5 of repeat IV .
 FT TRANSMEM 1762 1786 S6 of repeat IV .
 FT REPEAT 110 454 I .
 FT REPEAT 750 1022 II .
 FT REPEAT 1200 1514 III .
 FT REPEAT 1523 1821 IV .
 FT CARBOHYD 211 211 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 284 284 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 295 295 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 301 301 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 306 306 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 338 338 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 601 601 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 621 621 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 681 681 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 892 892 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1060 1060 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1064 1064 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1080 1080 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1146 1146 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1378 1378 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1392 1392 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 1403 1403 N-linked (GlcNAc . . .) (Potential) .
 SQ SEQUENCE 2009 AA; 228770 MW 6808466F6368373B CRC64;

Query Match 98.6% Score 10258; DB 1; Length 2009;
 Best Local Similarity 98.2% Pred. No. 0;
 Matches 1972; Conservative 24; M smatches 13; Indel s 0; Gaps 0;

Qy 1 MEQTVLVPPGPDSFNFFTRSLAAI ERRI AEEKAKNPKPDKKDDENGPKPNSDLEAGKN 60
 |||||
 Db 1 MEQTVLVPPGPDSFNFFTRSLAAI ERRI AEEKAKNPKPDKKDDENGPKPNSDLEAGKN 60
 Qy 61 LPFI YGDI PPEMSEPLEDLDPYYI NKKTFI VLNKGKAI FRFSATSALYI LTPFNPLRKI 120
 |||||
 Db 61 LPFI YGDI PPEMSEPLEDLDPYYI NKKTFI VLNKGKAI FRFSATSALYI LTPFNPLRKI 120

Qy	121	AI KI LVHSLF SMLI MCTI LTNCVFMTMSNPPDWTKNVEYFTFGI YTFESLI KI I ARGFCL	180
Db	121	AI KI LVHSLF SMLI MCTI LTNCVFMTMSNPPDWTKNVEYFTFGI YTFESLI KI I ARGFCL	180
Qy	181	EDFTFLRDPWVWLDFTVI TFAYVTEFVDLGNVSALRTFRVLRALKTI SVI PGLKTI VGAL	240
Db	181	EDFTFLRDPWVWLDFTVI TFAYVTEFVDLGNVSALRTFRVLRALKTI SVI PGLKTI VGAL	240
Qy	241	I QSVKKLSDVM LTVFCLSVFALI GLQLFMGNLRNKCI QWPPTNASLEEHSI EKNI TVNY	300
Db	241	I QSVKKLSDVM LTVFCLSVFALI GLQLFMGNLRNKCVQWPPTNASLEEHSI EKNVTTDY	300
Qy	301	NGTLI NETVFEFDWKS YI QDSRYHYFLEGFLDALLCGNSSDAGQCPEGYMCVKAGFNPNY	360
Db	301	NGTLVNETVFEFDWKS YI QDSRYHYFLEGVLDALLCGNSSDAGQCPEGYMCVKAGFNPNY	360
Qy	361	GYTSFDTFSWAFSLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA	420
Db	361	GYTSFDTFSWAFSLSLFRLMTQDFWENLYQLTLRAAGKTYM FFVLVI FLGSFYLI NLI LA	420
Qy	421	VVAMAYEEQNQATLEEAQEKEAEFQOM EQKKQQAACQAAATATASEHSREPSAAGRLS	480
Db	421	VVAMAYEEQNQATLEEAQEKEAEFQOMLEQKKQQAACQAAAAATASEHSREPSAAGRLS	480
Qy	481	DSSSEASKLSSKSAKERFRNRKRRKQKEQSGGEEKDEDEFQKSESEDSI RRKGRFSI EG	540
Db	481	DSSSEASKLSSKSAKERFRNRKRRKQKEQSGGEEKDDDEFHKSESEDSI RRKGRFSI EG	540
Qy	541	NRLTYEKRYSSPHQSLLSI RGSLSFSPRRNSRTSLFSFRGRAKDVGSENFADDEHSTFED	600
Db	541	NRLTYEKRYSSPHQSLLSI RGSLSFSPRRNSRTSLFSFRGRAKDVGSENFADDEHSTFED	600
Qy	601	NESRRDSL FVPRRHGERFRNSNL SQT SRSSRLAVFPANGKMHSTVDCNGV VSLVGGPSVP	660
Db	601	NESRRDSL FVPRRHGERFRNSNL SQT SRSSRLAGLPANGKMHSTVDCNGV VSLVGGPSVP	660
Qy	661	TSPVQQLLPEVI I DKPATDDNGTTTETEMRKRRSSSFHVSMDFLEDPSQRGRAMSI ASI L	720
Db	661	TSPVQQLLPEVI I DKPATDDNGTTTETEMRKRRSSSFHVSMDFLEDPSQRGRAMSI ASI L	720
Qy	721	TNTVEELEESRQKPPCWYKFSNI FLI WDCSPYWLKVKHVNLVVMDFVDLAI TI CI VL	780
Db	721	TNTVEELEESRQKPPCWYKFSNI FLI WDCSPYWLKVKHI VNLVVMDFVDLAI TI CI VL	780
Qy	781	NTLFVAMEHYPMTEHFNNVLTVGNLVFTGI FTAEMFLKI I AMDPYYYFQEGWNI FDGFI V	840
Db	781	NTLFVAMEHYPMTEHFNVHLTVGNLVFTGI FTAEMFLKI I AMDPYYYFQEGWNI FDGFI V	840
Qy	841	TLSSLVELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTLVLAI I	900
Db	841	TLSSLVELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLI KI I GNSVGALGNLTLVLAI I	900
Qy	901	VFI FAVVGIVLFGKSYKDCVCKI ASDCQLPRWHMNDFFHSFLI VFRVLOGEW ETMNDOM	960
Db	901	VFI FAVVGIVLFGKSYKDCVCKI ATDCKLPRWHMNDFFHSFLI VFRVLOGEW ETMNDOM	960
Qy	961	EVAGQAMCLTVFMMWMI GNLVVLNLFLALLLSSFSADNLAATDDDNEMNNLQI AVDRMH	1020
Db	961	EVAGQAMCLTVFMMWMI RNLVVLNLFLALLLSSFSADNLAATDDDNEMNNLQI AVDRMH	1020
Qy	1021	KGVAYVKRKI YEFI QGSFI RKQKI LDEI KPLDDLNNKKDSQMSNHTAEI GKDL DYLKDVN	1080

Db 1021 KGVAYVKRKI YEFI QGSFVRKQKI LDEI KPLDDLNNRKDNCTSNHTTEI GKDL DCLKDVN 1080
 Qy 1081 GTTSGI GTGSSVEKYI I DESDYMSFI NNPSLTVTVPI AVGESDFENLNTEDFSSES DLEE 1140
 Db 1081 GTTSGI GTGSSVEKYI I DESDYMSFI NNPSLTVTVPI AVGESDFENLNTEDFSSES DLEE 1140
 Qy 1141 SKEKLNESSSSSEGSTVDI GAPVEEQPVVEPEETLEPEACFTEGCVQRFKCCQI NVEEGR 1200
 Db 1141 SKEKLNESSSSSEGSTVDI GAPAEEQPVMEPEETLEPEACFTEGCVQRFKCCQI SVEEGR 1200
 Qy 1201 GKQWVNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
 Db 1201 GKQWVNLRRTCFRI VEHNWFETFI VFM LLSSGALAFEDI YI DQRKTI KTMLEYADKVFT 1260
 Qy 1261 YI FI LEMLLKWAYGYQTYFTNAWCVLDFLI VDVSLVSLTANALGYSELGAI KSLRTLRA 1320
 Db 1261 YI FI LEMLLKWAYGYQTYFTNAWCVLDFLI VDVSLVSLTANALGYSELGAI KSLRTLRA 1320
 Qy 1321 LRPLRALSRFEGMRVVVNALLGAI PSI MNVLLVCLI FWLI FSI MGVNLFAGKFYHCI NTT 1380
 Db 1321 LRPLRALSRFEGMRVVVNALLGAI PSI MNVLLVCLI FWLI FSI MGVNLFAGKFYHCVNTT 1380
 Qy 1381 TGDRFDI EDVNNHTDCLKLI ERNETARWKNVKVNF DNVGFGYLSLLQVATFKGWWDI MYA 1440
 Db 1381 TGDTFEI TEVNNHSDCLKLI ERNETARWKNVKVNF DNVGFGYLSLLQVATFKGWWDI MYA 1440
 Qy 1441 AVDSRNVELQPKYEESLYMYLYFVI FI I FGSFFTLNLFI GVI I DNFNQKKKKFGGQDI FM 1500
 Db 1441 AVDSRNVELQPKYEESLYMYLYFVI FI I FGSFFTLNLFI GVI I DNFNQKKKKFGGQDI FM 1500
 Qy 1501 TEEQKKYYNAMKKLGSKKPQKPI PRPGNKFQGMWDFVTRQVFDI SI M LI CLNMWMMW 1560
 Db 1501 TEEQKKYYNAMKKLGSKKPQKPI PRPGNKFQGMWDFVTRQVFDI SI M LI CLNMWMMW 1560
 Qy 1561 ETDDQSEYVTTI LSRI NLVFI VLFTGECVLKLI SLRHYYFTI GWN I FDFVWVI LSI VGMF 1620
 Db 1561 ETDDQSDYVTSI LSRI NLVFI VLFTGECVLKLI SLRHYYFTI GWN I FDFVWVI LSI VGMF 1620
 Qy 1621 LAELI EKYFVSPTLFRVI RLARI GRI LRLI KGAKGI RTLLFALMMSLPALFNI GLLLFLV 1680
 Db 1621 LAELI EKYFVSPTLFRVI RLARI GRI LRLI KGAKGI RTLLFALMMSLPALFNI GLLLFLV 1680
 Qy 1681 MFI YAI FGMSNFAYVKREVG I DDMFNFETFGNSM CLFQI TTSAGWDGLLAPI LNSKPPD 1740
 Db 1681 MFI YAI FGMSNFAYVKREVG I DDMFNFETFGNSM CLFQI TTSAGWDGLLAPI LNSKPPD 1740
 Qy 1741 CDPNKVNP GSSVKGDOGNPSVG I FFFVSYI I I SFLVVNM I AVI LENFSVATEESAEP L 1800
 Db 1741 CDPNKVNP GSSVKGDOGNPSVG I FFFVSYI I I SFLVVNM I AVI LENFSVATEESAEP L 1800
 Qy 1801 SEDDFEMFYEWKEKFDPDATQFMEFEKLSQFAAALEPPLNLPQPNKLQ I AMDLPWMSGD 1860
 Db 1801 SEDDFEMFYEWKEKFDPDATQFMEFEKLSQFAAALEPPLNLPQPNKLQ I AMDLPWMSGD 1860
 Qy 1861 RI HCLDI LFAFTKRVLGESGEMDALRI QMEERFMASNP SKVSYQPI TTTLKRKQEEVSAV 1920
 Db 1861 RI HCLDI LFAFTKRVLGESGEMDALRI QMEERFMASNP SKVSYQPI TTTLKRKQEEVSAV 1920
 Qy 1921 I I GRAYRRHLLKRTVKQASFTYNKNKI KGGANLLI KEDM I DRI NENSI TEKDLTMSTA 1980
 Db 1921 I I GRAYRRHLLKRTVKQASFTYNKNKI KGGANLLI KEDM I DRI NENSI TEKDLTMSTA 1980
 Qy 1981 ACPPSYDRVTKPI VEKHEQEGKDEKAKGK 2009

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Db 1981 ACPPSYDRVTKPI VEKHEQEGKDEKAKGK 2009

Search completed: June 5, 2008, 12:26:53
Job time : 2 secs